Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the instant application.

Listing of Claims

1. (original) A method for detecting a genetic abnormality on chromosome 12q15 in a patient, comprising:

obtaining a genetic sample from a patient;

producing a first reaction product by incubating the genetic sample with a polynucleotide, wherein the polynucleotide comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 123 to nucleotide 557;

(b) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 57 to nucleotide 557;

(c) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 21 to nucleotide 557; and

(d) polynucleotide sequence complementary to (a), (b) or (c),

wherein the incubation is under conditions wherein said polynucleotide will hybridize to a complementary polynucleotide sequence in the genetic sample;

visualizing the first reaction product; and

comparing said first reaction product to a control reaction product from a wild type patient, wherein a difference between said first reaction product and said control reaction product is indicative of a genetic abnormality on chromosome 12q15 in the patient.

2. (original) The method for detecting a genetic abnormality on chromosome 12q15 in a patient according to claim 1, wherein the polynucleotide consists of a polynucleotide selected from the group consisting of:

(a) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 123 to nucleotide 557;

(b) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 57 to nucleotide 557;

(c) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 21 to nucleotide 557; and

(d) a polynucleotide sequence complementary to (a), (b) or (c).

3. (original) The method according to claim 1, wherein the genetic abnormality further comprises a gross chromosomal abnormality, a translocation, aneuploidy, large insertion, large deletion, chromosome rearrangement, or a chromosome break at chromosome 12q15.

4. (original) A method for detecting a cancer in a patient, comprising:

obtaining a tissue or biological sample from a patient, wherein the biological sample contains a genetic sample;

labeling a polynucleotide, wherein the polynucleotide comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 123 to nucleotide 557;

(b) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 57 to nucleotide 557;

(c) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 21 to nucleotide 557; and

(d) a polynucleotide sequence complementary to (a), (b) or (c),

producing a first reaction product by incubating the tissue or biological sample with the labeled polynucleotide under conditions wherein the polynucleotide will hybridize to a complementary polynucleotide sequence in the tissue or biological sample;

visualizing the labeled polynucleotide; and

comparing said first reaction product to a control reaction product from a normal control tissue or biological sample, wherein a difference between said first reaction product and said control reaction product is indicative of a cancer in the patient.

5. (original) The method for detecting a cancer in a patient according to claim 4, wherein the difference between said first reaction product is an increase or decrease in the labeled polynucleotide hybridization to the patient tissue or biological sample, or the detection of a genetic abnormality on chromosome 12q15 in the patient tissue or biological sample, relative to the normal control tissue or biological sample.

6. (original) The method for detecting a cancer in a patient according to claim 4, wherein the difference between said first reaction product a genetic abnormality that further comprises a gross chromosomal abnormality, a translocation, aneuploidy, large insertion, large deletion, chromosome rearrangement, or a chromosome break at chromosome 12q15.

7. (original) The method for detecting a cancer in a patient according to claim 4, wherein the polynucleotide consists of a polynucleotide selected from the group consisting of:

(a) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 123 to nucleotide 557;

(b) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 57 to nucleotide 557;

(c) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 21 to nucleotide 557; and

(d) a polynucleotide sequence complementary to (a), (b) or (c).

8. (original) A method for detecting inflammation in a patient, comprising:

obtaining a tissue or biological sample from a patient;

labeling a polynucleotide, wherein the polynucleotide comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 123 to nucleotide 557;

(b) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 57 to nucleotide 557;

(c) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 21 to nucleotide 557; and

(d) a polynucleotide sequence complementary to (a), (b) or (c),

producing a first reaction product by incubating the tissue or biological sample with the labeled polynucleotide under conditions wherein the polynucleotide will hybridize to a complementary polynucleotide sequence in the tissue or biological sample;

visualizing the labeled polynucleotide in the tissue or biological sample; and

comparing the level of labeled polynucleotide hybridization in the tissue or biological sample from the patient to a normal control tissue or biological sample,

wherein a difference in the level in the labeled polynucleotide hybridization to the patient tissue or biological sample relative to the normal control tissue or biological sample is indicative of inflammation in the patient.

9. (original) The method for detecting inflammation in a patient according to claim 8, wherein the polynucleotide consists of a polynucleotide selected from the group consisting of:

(a) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 123 to nucleotide 557;

(b) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 57 to nucleotide 557;

(c) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 21 to nucleotide 557; and

(d) a polynucleotide sequence complementary to (a), (b) or (c).

10. (original) The method according to claim 8, wherein the tissue or biological sample from a patient comprises lymphoid cells, platelets, granulocytes, or neutrophils.

11. (Currently Amended) The method according to claim 8, wherein the inflammation is caused from an inflammatory disease comprising arthritis, asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, pancreatitis, sepsis, or endotoxemia.

12. (Currently Amended) A method for detecting activated T-cells in a patient suffering from inflammation, comprising:

obtaining a tissue or biological sample from a patient;

labeling a polynucleotide, wherein the polynucleotide comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 123 to nucleotide 557;

(b) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 57 to nucleotide 557;

(c) a polynucleotide sequence as shown in SEQ ID NO:1 from nucleotide 21 to nucleotide 557; and

(d) a polynucleotide sequence complementary to (a), (b) or (c),

producing a first reaction product by incubating the tissue or biological sample with the labeled polynucleotide under conditions wherein the polynucleotide will hybridize to a complementary polynucleotide sequence in the tissue or biological sample;

visualizing the labeled polynucleotide in the tissue or biological sample; and

comparing the level of labeled polynucleotide hybridization in the tissue or biological sample from the patient to a normal control tissue or biological sample,

wherein an increase in the labeled polynucleotide hybridization to the patient tissue or biological sample relative to the normal control tissue or biological sample is indicative of activated T-cells in the patient.

13. (original) The method according to claim 12, wherein the activated T-cells are CD3+ T-cells.

14. (Currently Amended) The method according to claim 12, wherein the inflammation is caused from an inflammatory disease comprising arthritis, asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, pancreatitis, sepsis, or endotoxemia.